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Human Brain Glycogen Phosphorylase

CLONING, SEQUENCE ANALYSIS, CHROMOSOMAL MAPPING, TISSUE EXPRESSION, AND COMPARISON WITH THE HUMAN LIVER AND MUSCLE ISOZYMES*

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We have cloned the cDNA encoding a new isozyme of glycogen phosphorylase (1,4,5-glucan:orthophosphate d-glucosyltransferase, EC 2.4.1.1) from a cDNA library prepared from a human brain astrocytoma cell line. Dot-blot hybridization analysis reveals that this message is preferentially expressed in human brain, but is also found at a low level in human fetal liver and adult liver and muscle tissues. Although previous studies have suggested that the major isozyme of phosphorylase found in all fetal tissues is the brain type, our data show that the predominant mRNA in fetal liver (24-week gestation) is the adult liver form.

The protein sequence deduced from the nucleotide sequence of the brain phosphorylase cDNA is 862 amino acids long compared with 846 and 841 amino acids for the liver and muscle isozymes, respectively; the greater length of brain phosphorylase is entirely due to an extension at the far C-terminal portion of the protein. The muscle and brain isozymes share greater identity with regard to nucleotide and deduced amino acid sequences, codon usage, and nucleotide composition than either do with the liver sequence, suggesting a closer evolutionary relationship between them. Spot blot hybridization of the brain phosphorylase cDNA to laser-sorted human chromosome fractions, and Southern blot hybridization of the brain phosphorylase cDNA to human brain phosphorylase RNA reveals that the exact homolog of the newly cloned cDNA maps to chromosome 20, but that a slightly less homologous gene is found on chromosome 10 as well. The liver and muscle genes have previously been localized to chromosomes 14 and 11, respectively. This suggests that the phosphorylase genes evolved by duplication and translocation of a common ancestral gene, leading to divergence of elements controlling gene expression and of structural features of the phosphorylase proteins that confer tissue-specific functional properties.

Mammalian glycogen phosphorylases are found in at least three isozymic forms that can be distinguished by functional and structural properties as well as by the tissues in which they are preferentially expressed (1-5). A brain form has been described previously as the predominant isozyme in adult brain and most fetal tissues, whereas adult liver and muscle tissues are known to express primarily the liver and muscle isozymes, respectively. Each phosphorylase isozyme fulfills different physiological requirements even though all forms of the enzyme catalyze the same reaction, the phosphorylisis of glycogen to yield glucose 1-phosphate. The muscle enzyme provides metabolic fuel for muscular contraction, the liver form plays a central role in the maintenance of blood glucose homeostasis, and the brain type is associated primarily with provision of an emergency glucose supply during periods of anoxia or hypoglycemia. Phosphorylase isozymes exhibit differences in regulatory properties that may be related to their distinct physiological roles, especially with regard to their response to the allosteric ligand AMP.

The cDNAs encoding rabbit muscle and human liver glycogen phosphorylases, as well as the gene for the human muscle form, have been cloned and sequenced (5-8). In addition, the genes for muscle and liver phosphorylase have been localized to human chromosomes 11 and 14, respectively (9, 10). The crystal structure of rabbit muscle phosphorylase has allowed us to identify and characterize the active site and five allosteric sites of this enzyme (11, 12). Using this structure, we have identified amino acid substitutions predicted by the liver phosphorylase cDNA sequence that may be involved in specifying functional differences between the liver and muscle isozymes (13).

In this report we describe the cloning and sequence analysis of the cDNA encoding an isozyme of glycogen phosphorylase that is preferentially expressed in adult human brain tissues (hereafter referred to as the "brain" isozyme). The cloning of this cDNA has allowed us to 1) analyze and compare the expression of the brain and liver phosphorylase messenger RNAs in human adult brain, liver, and muscle tissues, as well as human fetal liver tissues, 2) map the brain phosphorylase gene to chromosome 20 and a homologous gene to chromosome 10, thus demonstrating that the human phosphorylase genes are unlinked, and 3) compare the human brain phosphorylase cDNA and predicted protein sequences with their human muscle and liver counterparts, thereby gaining insight into structural and evolutionary relationships among the three isozymes.

MATERIALS AND METHODS

Construction of a Human Brain Astrocytoma cDNA Library—Poly(A)* RNA isolated from the human astrocytoma cell line U251...
was used to synthesize double-stranded cDNA using oligo(dT) as the first strand primer. Actinomycin D (40 μg/ml) was included during first-strand synthesis to reduce hairpin formation. The second strand was synthesized by the procedure of Okayama and Berg (14) using RNAse H and Escherichia coli DNA polymerase and DNA ligase. The cDNAs were treated with EcoRI methylase and S-adenosylmethionine. T4 DNA polymerase was used to generate blunt ends. After ligating EcoRI linkers to the ends, the cDNAs were digested with EcoRI and separated on a 1.5% agarose gel. cDNAs greater than 1.5 kb in length were inserted into the EcoRI site of Xgt10 (15).

Panel A of Fig. 1 shows the restriction pattern obtained for the former class of clones consistent with that described previously for the full-length liver phosphorylase cDNA. The size of the latter class of clones (3.47 kb + 3.47 kb + 0.35 kb) seemed to preclude the possibility that they represent liver or muscle phosphorylase mRNAs, since previous Northern blot analysis has sized these messages at 3.2 and 3.4 kb, respectively, in rabbit tissues (5). The 0.35-kb EcoRI fragment was ligated into the sequencing vector M13, and the larger fragment was subcloned according to the strategy depicted in Fig. 1. Dideoxynucleotide sequencing of these cloned fragments shows that they correspond to a phosphorylase isozyme with a nucleotide and deduced amino acid sequence distinct from the human liver and muscle phosphorylase sequences (see below).

Northern blot hybridization analysis was undertaken in order to characterize the tissue expression pattern of the newly isolated phosphorylase clone and to compare it with the pattern obtained with the liver phosphorylase cDNA. Poly(A)+ mRNA was prepared from human adult brain, muscle, and liver and 24-week-old fetal liver tissues, as well as the astrocytoma cell line U251. Panel A of Fig. 2 shows the hybridization pattern obtained when the liver phosphorylase cDNA was used to probe filters containing these types of RNA. Strong hybridization to a 3.2-kb mRNA is observed in both adult and fetal liver tissues (lanes L and FL). The liver probe also detects an identically sized message in U251 RNA and a slightly larger (approximately 3.4 kb) message in adult muscle. The latter likely represents cross-hybridization to the muscle-specific phosphorylase mRNA since this message is identical in size with that seen in rabbit muscle tissues when probing with the rabbit muscle phosphorylase cDNA; hybridization of the latter class of clones to human liver and muscle tissues was not observed. Northern and Southern blot analysis of the U251 and human liver and muscle tissues was performed to confirm the identity of the 3.2-kb mRNA as phosphorylase.

The restriction enzymes EcoRI (R), SacI (S), BamH1 (B), and PstI (P) were used to subclone fragments of the brain phosphorylase cDNA into M13 (strains MP 18 and MP 19) as shown. Protein-encoding regions of the cDNA are depicted by the dark bar, untranslated regions are shown as lines. The distance of each restriction site from the 5' end of the clone is given in kilobases (kb) directly under the map, and below that, arrows indicate the direction and distance over which each fragment was sequenced. The two small boxes centered under the 3'-untranslated region of the cDNA indicate two oligonucleotides used as sequencing primers due to the absence of any convenient restriction sites in this area.

1 The abbreviations used are: kb, kilobase(s); SDS, sodium dodecyl sulfate.
that most human tissues express more than one type of mRNA. In particular, the temporal lobe of human brain expresses significant amounts of liver phosphorylase mRNA, in contrast to the rabbit, where no liver phosphorylase mRNA is detectable in whole brain extracts (5). The reasons for having more than one phosphorylase mRNA expressed in a given tissue are unclear, especially since the current results do not conform well to earlier protein electrophoresis studies that showed no liver phosphorylase activity in human brain extracts or brain phosphorylase activity in liver or muscle tissues (21). The final and perhaps most interesting observation is that the predominant mRNA present in 24-week-old (midgestation) fetal liver is the adult liver form; the brain-type RNA is present at the same low constitutive level in both fetal and adult liver and in adult human muscle tissues. There are several possible explanations for the discrepancies between the current data and those pertaining to the developmental expression profile of phosphorylase isozymes in rat: 1) human fetal liver, unlike rat fetal liver, contains primarily the adult liver isozyme of phosphorylase (a possibility that has also been implied by previous investigators (21)); 2) in human fetal liver, the liver gene is actively transcribed but inefficiently translated, whereas the small amount of brain phosphorylase message is rapidly translated; or 3) the human brain isozyme only predominates in early fetal liver development and is replaced by the adult liver isozyme well before birth. The current data cannot discriminate among these possibilities, nor do they suggest that the brain isozyme is not predominantly expressed in other human fetal tissues. With three cDNA clones in hand, it will now be possible to address developmental expression of phosphorylase isozymes in more detail.

The nucleotide and deduced amino acid sequence of the three human phosphorylase isozymes, brain (this work), liver (5), and muscle (8) are shown in Fig. 3. The protein predicted by the brain phosphorylase cDNA sequence is 862 amino acids long with a molecular mass of 112,917 daltons, a value in close agreement with that previously determined by gel electrophoresis for the rat brain phosphorylase monomer (24). In contrast, human muscle and liver phosphorylase contain 841 and 846 amino acids, respectively. The increased size of the brain phosphorylase protein is entirely due to insertion of amino acids at the C terminus; the three human phosphorylase isozymes can be aligned without insertions or deletions so that amino acids 1–830 match. Previous workers have often resolved phosphorylase isozymes by using slab or disc polyacrylamide electrophoresis in the absence of SDS; under these conditions, the brain isozyme is usually described as a “faster migrating band” than the liver or muscle types (1–4, 20, 21). We have determined that the isoelectric point predicted by the primary sequence of brain phosphorylase is 6.15, as compared to 6.24 and 6.42 for the liver and muscle phosphorylase isozymes, respectively, values consistent with the previously observed electrophoretic patterns.

The brain phosphorylase amino acid sequence is 83% identical to the muscle sequence and 80% identical to the liver sequence. The liver and muscle sequences are also 80% identical. Thus, the sequences of the human muscle and brain phosphorylase isozymes are more closely related than either are to the liver isozyme. The same is true at the nucleotide level where the identities are 79% for the brain/muscle comparison, versus 74% (brain/liver) and 73% (muscle/liver). Fig. 3 also provides the sequence of 80 bases of 5′-untranslated region and all of the 3′-untranslated region of the brain phosphorylase cDNA. Whereas the liver and muscle 5′-untranslated sequences have been shown to be approximately

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**Fig. 2. Tissue distribution of glycogen phosphorylase mRNA in human tissues, assessed with liver and brain phosphorylase cDNA probes.** Filters containing poly(A+) RNA were hybridized with radiolabeled liver phosphorylase cDNA (panel A) or brain phosphorylase cDNA (panel B) probes, as described under "Materials and Methods." Lanes: BT, 10 μg of poly(A+) RNA isolated from the temporal lobe of adult brain; BF, 2 μg of poly(A+) RNA isolated from the frontal lobe of adult brain; FL, 5 μg of poly(A+) RNA isolated from 24-week-old fetal liver; L, 5 μg of poly(A+) RNA isolated from adult liver; M, 2 μg of poly(A+) RNA isolated from adult skeletal muscle (call); U251, 5 μg of poly(A+) RNA isolated from the human brain astrocytoma cell line from which the cDNA library was derived.
**Human Brain Phosphorylase**

![DNA sequence and amino acid alignment](image)

Fig. 3. DNA and deduced amino acid sequences of human brain (this work), liver (5), and muscle (8) isoforms of glycogen phosphorylase. The numbers above the brain sequence indicate the amino acid number, with the residues immediately after the initiator methionine (glycine in brain and liver phosphorylase, serine in muscle) designated number 1. The brain phosphorylase amino acid and nucleotide sequences are presented in their entirety in the first and fourth lines of each row, respectively, except for the 5’- and 3’-untranslated regions, where the brain nucleotide sequence is found in the first line of the row. The brain sequence serves as the reference sequence; only nucleotide and amino acid residues that are nonidentical in the liver and muscle sequences are underlined.

The polyadenylation signals AATAAA (liver and muscle) or ATTAAA (brain) are in their entirety in the first and fourth lines of each row, respectively, except for the 5’- and 3’-untranslated regions, where the brain nucleotide sequence is found in the first line of the row. The brain sequence serves as the reference sequence; only nucleotide and amino acid residues that are nonidentical in the liver and muscle sequences are underlined.

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63% identical (5), the brain sequence appears to be unrelated to the other two. The greater length of the brain phosphorylase mRNA detected on Northern blots is largely attributable to the much longer 3' untranslated region of the brain phosphorylase cDNA (1147 base pairs) as compared to the liver (170 base pairs) and muscle (263 base pairs) sequences. The longer 3'-untranslated region of the brain phosphorylase cDNA is a feature shared with the brain isoforms of two other isozyme families, Na⁺K⁺-ATPase and protein kinase C (25, 26). The cDNA encoding brain aldolase, in contrast, has a 3'-untranslated region of similar length to that found for the liver and muscle forms. The 3'-untranslated region of the brain cDNA contains 57% G + C compared with 55% for the muscle and 28% for the liver messages. In addition to this similarity in nucleotide composition, the brain and muscle messages have a nearly identical 11-nucleotide sequence, CTGCGAGCGA\(^3\). This sequence was previously shown to be located at amino acid 833 of the muscle phosphorylase sequence, exactly conserved among rat, rabbit, and human muscle phosphorylase cDNAs (6), leading to the suggestion that it may play a role in regulation of muscle phosphorylase gene expression. The sequence appears in the brain message 90 nucleotides into the 3'-untranslated region, but is not found in any region of the liver phosphorylase cDNA. No other regions of significant sequence identity are observed when comparing the 3' ends of the muscle and brain phosphorylase cDNAs. This finding, coupled with the abrupt divergence of the three phosphorylase sequences surrounding amino acid 830, suggests that the muscle and brain genes evolved in an otherwise conserved region of the 5'-untranslated region since no primer extension or S1 mapping was done to define the 5' end. Note that we have assumed that translation initiates at the methionine codon in the brain phosphorylase cDNA corresponding to the start site in the other two sequences. This seems likely since 1) no other ATG codons are found in the 80 nucleotides upstream of this site in the brain sequence, 2) the protein predicted by the open reading frame that begins at this site is 112,917 daltons, in exact agreement with the estimated molecular mass of the brain phosphorylase monomer (24), and 3) the amino acid residues 1-14 have been shown to be important in the covalent modification of muscle phosphorylase by phosphorylation and dephosphorylation (12). Since brain phosphorylase is recognized by muscle phosphorylase kinase, it is unlikely that any modification (elongation) has occurred at the N terminus.

FIG. 3—continued

We have compared previously the human liver and rabbit muscle phosphorylase cDNA and predicted protein sequences (5). That study demonstrated that despite an 80% amino acid identity, two distinct patterns of codon usage were used to encode these proteins, i.e. the rabbit muscle phosphorylase cDNA was shown to have a significantly higher proportion of deoxyguanosine (G) and deoxycytosine (C) residues at third codon positions (86%) than its human liver counterpart (60%). Based on the data in Fig. 3, we can now calculate a third position G + C content of 77% for the human muscle and 82% for the human brain coding sequences. Furthermore, the overall G + C content of the coding sequences of the three messages is 49% for liver, 57% for muscle, and 59% for brain. This analysis provides a further indication that the brain and muscle genes have a closer evolutionary relationship to each other than to the liver gene.

Some gene families (such as those for the globins or some of the serine proteases) are found grouped together in tandem array, implicating an evolutionary mechanism involving gene duplication and retention of the gene copies on a single chromosome. This strategy does not apply to the phosphorylase gene family. We have shown previously that the genes for human muscle and liver phosphorylase map to chromosomes 11 and 14, respectively, by hybridizing the appropriate DNA probes to laser-sorted human chromosomal fractions spotted onto nitrocellulose (9, 10). Fig. 4 depicts the results of this kind of chromosome mapping experiment performed with the human brain phosphorylase cDNA probe. Strong hybridization is seen to the spot containing chromosome 20. A lesser

FIG. 4. Assignment of the brain phosphorylase gene to human chromosome 20. Autoradiograph of a panel of nitrocellulose filters, each with two fractions of flow-sorted human chromosomes as numbered. The chromosomal DNA was denatured and hybridized to a radiolabeled 3.47 EcoRI fragment of brain phosphorylase cDNA (see Fig. 1) as described in Ref. 10.

\(^2\) The difference in size between the brain phosphorylase mRNA depicted in Fig. 2 (~4.2 kb) and the brain phosphorylase cDNA clone described in Fig. 3 (3.82 kb) is presumably due to the lack of a poly(A) tail in the latter. Some of the difference may also be due to unsequenced regions of the 5'-untranslated region since no primer extension or S1 mapping was done to define the 5' end. Note that we have assumed that translation initiates at the methionine codon in the brain phosphorylase cDNA corresponding to the start site in the other two sequences. This seems likely since 1) no other ATG codons are found in the 80 nucleotides upstream of this site in the brain sequence, 2) the protein predicted by the open reading frame that begins at this site is 112,917 daltons, in exact agreement with the estimated molecular mass of the brain phosphorylase monomer (24), and 3) the amino acid residues 1-14 have been shown to be important in the covalent modification of muscle phosphorylase by phosphorylation and dephosphorylation (12). Since brain phosphorylase is recognized by muscle phosphorylase kinase, it is unlikely that any modification (elongation) has occurred at the N terminus.

\(^3\) D. Tolan, personal communication.
whether the gene on chromosome 10 is an expressed or phorylase cDNA cloned in this study maps to chromosome vocably distinguish between chromosomes 9, 10, 11, and 12; a that the gene with exact homology to the human brain phos- mapping studies using DNA purified from hamster/human on chromosome 10. It is unclear from the current study some 20, but also reveal the presence of a somewhat less distinguish among these possibilities, we carried out further cross-hybridization with the muscle phosphorylase gene on one of two ways. It is either due to the larger amount of DNA on this spot than on any other and/or a small amount of specific phosphorylase cDNAs. The results, shown in Fig. 5 confirm the strong hybridization to a gene found on chromo- some 20, but also reveal the presence of a somewhat less homologous fragment on chromosome 10. Thus, we conclude that the gene with exact homology to the human brain phos- phorylase cDNA cloned in this study maps to chromosome 20, but that a gene encoding a very similar sequence is found in different tissues are derived from one or the other of the brain genes, since the latter have retained greater similarities to fit each isozyme's physiological role. Sequence analysis of phosphorylase isozymes has led to insights into the evolution of al- logenic regulatory properties tailored to each isozyme's physiological role. Sequence analysis of phosphorylase isozymes can be stimulated by innervation to produce the mature muscle isozyme (32) suggests that cell culture techniques or the heterokaryon approach of Blau and associates (33) will be useful for defining the regions of the various phosphorylase genes that are involved in gene regulation. To this end, we are currently isolating the liver and brain phos- phorylase genes, using our cDNA clones as probes.

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Fig. 5. Resolution of chromosomes 9, 10, 11, and 12 by southern blot analysis of hamster/human hybrid cell line DNA. The filter contains 10 µg of hamster genomic DNA (lane 1) or 20 µg of DNA isolated from various hamster/human hybrid cell lines (lanes 2–8) digested to completion with EcoRI. It was probed with a 1.1-kb PstI/EcoRI fragment derived from the 3'-untranslated region of the brain-specific cDNA (see Fig. 1), since this region has no homolog in the muscle- or liver-specific phosphorylase cDNAs. The results, shown in Fig. 5 confirm the strong hybridization to a gene found on chromosome 20, but also reveal the presence of a somewhat less homologous fragment on chromosome 10. Thus, we conclude that the gene with exact homology to the human brain phosphorylase cDNA cloned in this study maps to chromosome 20, but that a gene encoding a very similar sequence is found on chromosome 10. It is unclear from the current study whether the gene on chromosome 10 is an expressed or pseudogene. There is no evidence for multiple mRNA bands in Fig. 3B; given the high homology of the two genes, however, it cannot be ruled out that the "brain like" transcripts found in different tissues are derived from one or the other of the brain like genes. The issue will be resolved in future studies in which the transcripts in the cell lines containing either chromosome 10 or 20 will be analyzed.

Clearly, the genes encoding the tissue-specific isozymes of phosphorylase are unlinked. It has been suggested that the genes encoding tissue-specific forms of aldolase are found on separate chromosomes because of tetraploidization, since re- lated aldolase genes are found on morphologically similar chromosomes (aldolases A and C on chromosomes 16 and 17, aldolase B and an aldolase pseudogene on chromosomes 9 and 10) (27). The localization of the phosphorylase genes to three morphologically unrelated chromosomes thus would appear to involve a more specific translocation mechanism. Our data suggest that the liver phosphorylase gene has evolved by a route distinct from that taken by the muscle and brain genes, since the latter have retained greater similarities in primary sequence, codon usage, and nucleotide composi- tion. Interestingly, the muscle and brain phosphorylase gene products are also more responsive to the allosteric effector AMP than the liver protein, although AMP activation does not appear to be cooperative in brain phosphorylase as it is in the muscle form (28, 29). It is reasonable to assume that the phosphorylase genes were duplicated and dispersed in the genome, leading to the evolution of regulatory elements controlling tissue-specific and developmental patterns of gene expression, as well as allosteric regulatory properties tailored to fit each isozyme's physiological role. Sequence analysis of phosphorylase isozymes has led to insights into the evolution of al- logenic regulatory properties tailored to each isozyme's physiological role. Sequence analysis of phosphorylase isozymes can be stimulated by innervation to produce the mature muscle isozyme (32) suggests that cell culture techniques or the heterokaryon approach of Blau and associates (33) will be useful for defining the regions of the various phosphorylase genes that are involved in gene regulation. To this end, we are currently isolating the liver and brain phos- phorylase genes, using our cDNA clones as probes.
Human Brain Phosphorylase


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